

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/729,571C  
Source: 1 Fw/b  
Date Processed by STIC: 10/20/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/729,571C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4        Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)         SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi)        SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
  
- 11        Use of <220>     Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

3 <110> APPLICANT: Anderson et al.  
 5 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE (MURI)  
 7 <130> FILE REFERENCE: 100966  
 9 <140> CURRENT APPLICATION NUMBER: US 10/729,571C  
 10 <141> CURRENT FILING DATE: 2003-12-05  
 12 <150> PRIOR APPLICATION NUMBER: 60/435,272  
 13 <151> PRIOR FILING DATE: 2002-12-20  
 15 <150> PRIOR APPLICATION NUMBER: 60/435,167  
 16 <151> PRIOR FILING DATE: 2002-12-20  
 18 <150> PRIOR APPLICATION NUMBER: 60/435,087  
 19 <151> PRIOR FILING DATE: 2002-12-20  
 21 <150> PRIOR APPLICATION NUMBER: 60/435,527  
 22 <151> PRIOR FILING DATE: 2002-12-20  
 E--> 24 <160> NUMBER OF SEQ ID NOS: 76 97 (see p. 22)  
 26 <170> SOFTWARE: PatentIn version 3.1

*error throughout*

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES

28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 768  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: H. pylori  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (1)..(768)  
 E--> 36 <400> SEQUENCE: 1  
 37 atg aaa ata ggc gtt ttt gat agc ggt gtg ggg ggg ttt agc gtt tta  
 38 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 39 1 5 10 15  
 41 aaa agc ctt tta aaa gcg cga ttg ttt gat gaa atc atc tac tat ggc  
 42 Lys Ser Leu Leu Lys Ala Arg Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 43 20 25 30  
 45 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag  
 46 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 47 35 40 45  
 49 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cat gag att gaa  
 50 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu  
 51 50 55 60  
 53 tta ttg att gtg gca tgc aac acc gcg agc gct ctg gct tta gaa gag  
 54 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 55 65 70 75 80  
 57 atg caa aag tat tct aaa atc cct att gtg ggc gtg att gag cca agc  
 58 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser

*insert  
<220>*

*insert <220>  
wherever <221>, <222>, or <223> is  
shown*

*<220> is  
a "header"  
only. it  
never has a  
response.*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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59          85          90          95
61 att tta gcg atc aag cgg caa gtg gaa gat aaa aac gcc cct att tta      336
62 Ile Leu Ala Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu
63          100          105          110
65 gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gac aac gcc      384
66 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
67          115          120          125
69 ctg aaa caa caa ggc tat ttg aac att tcg cat tta gct act tct ctt      432
70 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
71          130          135          140
73 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
74 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
75 145          150          155          160
77 act tgc atg cat tat tat ttc act ccc tta gag att tta ccc gaa gtg      528
78 Thr Cys Met His Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
79          165          170          175
81 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
82 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
83          180          185          190
85 ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
86 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
87          195          200          205
89 cat tcg ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
90 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
91          210          215          220
93 aaa aac aat gca tgc aca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
94 Lys Asn Asn Ala Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly
95 225          230          235          240
97 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa      768
98 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
99          245          250          255
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 768
173 <212> TYPE: DNA
174 <213> ORGANISM: H. pylori
176 <221> NAME/KEY: CDS
177 <222> LOCATION: (1)..(768)
179 <400> SEQUENCE: 3
180 atg aaa ata ggc gtt ttt gat agc ggt gtg ggg ggg ttt agc gtt tta      48
181 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
182 1          5          10          15
184 aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc      96
185 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
186          20          25          30
188 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag      144
189 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
190          35          40          45
192 caa ttt ggc tta gag gct ttg gat ttt ttc aaa cca cac cag att gaa      192
193 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu

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OK

insert  
 (2207)

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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194      50      55      60
196 tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag      240
197 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
198 65      70      75      80
200 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
201 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
202      85      90      95
204 att tta gcg atc aag caa caa gtg aaa gat aaa aac gcc cct att tta      336
205 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
206      100      105      110
208 gtg cta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc      384
209 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
210      115      120      125
212 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
213 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
214      130      135      140
216 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag      480
217 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
218 145      150      155      160
220 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
221 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
222      165      170      175
224 att att tta ggt tgc acg cat ttt ccc ttg att gct caa aaa att gag      576
225 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
226      180      185      190
228 ggc tat ttc atg gag cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
229 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
230      195      200      205
232 cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac gcc ctt      672
233 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
234      210      215      220
236 aaa aac aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
237 Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
238 225      230      235      240
240 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa      768
241 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
242      245      250      255

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314 &lt;210&gt; SEQ ID NO: 5

315 &lt;211&gt; LENGTH: 768

316 &lt;212&gt; TYPE: DNA

317 &lt;213&gt; ORGANISM: H. pylori

319 &lt;221&gt; NAME/KEY: CDS

320 &lt;222&gt; LOCATION: (1)..(768)

E--&gt; 322 &lt;400&gt; SEQUENCE: 5

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323 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
324 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
325 1      5      10      15
327 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
328 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly

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*insert 2207*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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329          20          25          30
331 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag      144
332 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
333          35          40          45
335 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa      192
336 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
337          50          55          60
339 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
340 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
341 65          70          75          80
343 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
344 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
345          85          90          95
347 att tta gcg atc aag cga caa gta aaa gat aaa aac gcc cct att tta      336
348 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
349          100          105          110
351 gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aat gcc      384
352 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
353          115          120          125
355 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
356 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
357          130          135          140
359 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
360 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
361 145          150          155          160
363 act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc gaa gtg      528
364 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
365          165          170          175
367 att att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
368 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
369          180          185          190
371 ggc tat ttt atg gag cat ttt gcc ctt tca aca ccc ccc cta ctc atc      624
372 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
373          195          200          205
375 cat tcg ggc gat gct att gta gga tat ttg cag caa aaa tac gcc ctt      672
376 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
377          210          215          220
379 aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
380 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
381 225          230          235          240
383 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
384 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
385          245          250          255
457 <210> SEQ ID NO: 7
458 <211> LENGTH: 749
459 <212> TYPE: DNA
460 <213> ORGANISM: H. pylori
462 <221> NAME/KEY: CDS
463 <222> LOCATION: (1)..(747)

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*insert 2207*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

## E--&gt; 465 &lt;400&gt; SEQUENCE: 7

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466 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
467 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
468 1          5          10          15
470 aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc      96
471 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
472          20          25          30
474 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
475 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
476          35          40          45
478 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
479 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
480          50          55          60
482 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
483 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
484 65          70          75          80
486 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
487 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
488          85          90          95
490 att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta      336
491 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
492          100          105          110
494 gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aac gcc      384
495 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
496          115          120          125
498 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
499 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
500          130          135          140
502 ttt gtg cct ttg att gaa gaa agt att tta ggg ggc gaa ttg tta gaa      480
503 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Gly Gly Glu Leu Leu Glu
504 145          150          155          160
506 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
507 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
508          165          170          175
510 att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
511 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
512          180          185          190
514 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
515 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
516          195          200          205
518 cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
519 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
520          210          215          220
522 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
523 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
524 225          230          235          240
526 gat gtg atc tgg cta gaa aaa cag gct aa      749
527 Asp Val Ile Trp Leu Glu Lys Gln Ala
528          245

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## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

600 <210> SEQ ID NO: 9  
 601 <211> LENGTH: 768  
 602 <212> TYPE: DNA  
 603 <213> ORGANISM: H. pylori  
 605 <221> NAME/KEY: CDS  
 606 <222> LOCATION: (1)..(768) *insert <220>*

E--> 608 <400> SEQUENCE: 9

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610	Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu	
611	1 5 10 15	
613	aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc	96
614	Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
615	20 25 30	
617	gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
618	Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
619	35 40 45	
621	caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga	192
622	Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly	
623	50 55 60	
625	tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag	240
626	Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
627	65 70 75 80	
629	atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc	288
630	Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser	
631	85 90 95	
633	att tta gcg atc aag caa caa gta aaa gat aaa aac gcc tct att ttg	336
634	Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Ser Ile Leu	
635	100 105 110	
637	gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aac gcc	384
638	Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
639	115 120 125	
641	ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt	432
642	Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu	
643	130 135 140	
645	ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa	480
646	Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu	
647	145 150 155 160	
649	act tgc atg cgt tat tat ttc act ccg tta gag atc ttg cct gaa gtg	528
650	Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val	
651	165 170 175	
653	gtt att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag	576
654	Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
655	180 185 190	
657	ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc	624
658	Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile	
659	195 200 205	
661	cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt	672
662	His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Lys Tyr Ala Leu	
663	210 215 220	



## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

665 aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc      720
666 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
667 225                230                235                240
669 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
670 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
671                245                250                255
743 <210> SEQ ID NO: 11
744 <211> LENGTH: 749
745 <212> TYPE: DNA
746 <213> ORGANISM: H. pylori
748 <221> NAME/KEY: CDS
749 <222> LOCATION: (1)..(747)
E--> 751 <400> SEQUENCE: 11
752 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
753 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
754 1                5                10                15
756 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
757 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
758                20                25                30
760 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
761 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
762                35                40                45
764 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
765 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
766                50                55                60
768 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
769 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
770 65                70                75                80
772 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
773 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
774                85                90                95
776 att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta      336
777 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
778                100               105               110
780 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc      384
781 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
782                115               120               125
784 cta aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt      432
785 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
786                130               135               140
788 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag      480
789 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
790 145               150               155               160
792 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
793 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
794                165               170               175
796 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
797 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
798                180               185               190

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*insert <2207*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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800 ggc tat ttt atg gag cat ttt gcc ctt cca acc ccc ccc cta ctc atc      624
801 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
802      195      200      205
804 cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac acc ctt      672
805 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
806      210      215      220
808 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc      720
809 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
810 225      230      235      240
812 gat gtg gtt tgg cta gaa aaa cag gct aa      749
813 Asp Val Val Trp Leu Glu Lys Gln Ala
814      245
886 <210> SEQ ID NO: 13
887 <211> LENGTH: 768
888 <212> TYPE: DNA
889 <213> ORGANISM: H. pylori
891 <221> NAME/KEY: CDS
892 <222> LOCATION: (1)..(768)
E--> 894 <400> SEQUENCE: 13
895 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
896 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
897 1      5      10      15
899 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
900 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
901      20      25      30
903 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
904 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
905      35      40      45
907 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga      192
908 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
909      50      55      60
911 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
912 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
913 65      70      75      80
915 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
916 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
917      85      90      95
919 att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta      336
920 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
921      100      105      110
923 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gcc      384
924 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
925      115      120      125
927 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
928 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
929      130      135      140
931 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa      480
932 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
933 145      150      155      160

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*insert 2207*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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935 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
936 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
937          165          170          175
939 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
940 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
941          180          185          190
943 ggc tat ttt atg gag cat ttt gcc ctt tta acg ccc ccc cta ctc atc      624
944 Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile
945          195          200          205
947 cat tct ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
948 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
949          210          215          220
951 aag aaa aat gca cac tca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
952 Lys Lys Asn Ala His Ser Phe Pro Lys Val Glu Phe His Ala Ser Gly
953 225          230          235          240
955 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
956 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
957          245          250          255
1029 <210> SEQ ID NO: 15
1030 <211> LENGTH: 768
1031 <212> TYPE: DNA
1032 <213> ORGANISM: H. pylori
1034 <221> NAME/KEY: CDS
1035 <222> LOCATION: (1)..(768)
E--> 1037 <400> SEQUENCE: 15
1038 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1039 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1040 1          5          10          15
1042 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
1043 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
1044          20          25          30
1046 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1047 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1048          35          40          45
1050 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa      192
1051 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
1052          50          55          60
1054 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1055 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1056 65          70          75          80
1058 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc      288
1059 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1060          85          90          95
1062 att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta      336
1063 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1064          100          105          110
1066 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gac aac gcc      384
1067 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1068          115          120          125

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*Insert <220>*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

1070 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
1071 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1072      130                      135                      140
1074 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa      480
1075 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1076 145                      150                      155                      160
1078 act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc aaa gta      528
1079 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val
1080                      165                      170                      175
1082 atc att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att aag      576
1083 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys
1084                      180                      185                      190
1086 ggc tat ttt atg ggg cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
1087 Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Leu Leu Ile
1088      195                      200                      205
1090 cat tcg ggc gat gct att gtg gga tat ttg caa caa aaa tac gcc ctt      672
1091 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
1092      210                      215                      220
1094 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1095 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1096 225                      230                      235                      240
1098 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1099 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1100      245                      250                      255
1172 <210> SEQ ID NO: 17
1173 <211> LENGTH: 768
1174 <212> TYPE: DNA
1175 <213> ORGANISM: H. pylori
1177 <221> NAME/KEY: CDS
1178 <222> LOCATION: (1)..(768)
E--> 1180 <400> SEQUENCE: 17
1181 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1182 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1183 1                      5                      10                      15
1185 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1186 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1187      20                      25                      30
1189 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1190 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1191      35                      40                      45
1193 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1194 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
1195      50                      55                      60
1197 tta ttg att gtg gca tgc aac aca gcg agt gct ctg gct tta gaa gag      240
1198 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1199 65                      70                      75                      80
1201 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1202 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1203      85                      90                      95

```

*insert (2207)*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1205 att tta gcg atc aaa caa cag gta aaa gat aaa aac gcc ccc att tta      336
1206 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1207           100                      105                      110
1209 gtg cta ggc aca aaa gcg acg att caa tct aac gct tac gat aac gct      384
1210 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1211           115                      120                      125
1213 ctg aaa cga caa ggc tat ttg aac gtt tcg cat tta gcc act tcc ctt      432
1214 Leu Lys Arg Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1215           130                      135                      140
1217 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
1218 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1219 145           150                      155                      160
1221 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
1222 Thr Cys Met Arg Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
1223           165                      170                      175
1225 atc att tta ggt tgt acg cat ttt ccc ttg atc gct caa aaa att gag      576
1226 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1227           180                      185                      190
1229 ggc tat ttt atg gaa cat ttt gcc ttt cca acg ccc ccc cta ctc atc      624
1230 Gly Tyr Phe Met Glu His Phe Ala Phe Pro Thr Pro Pro Leu Leu Ile
1231           195                      200                      205
1233 cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1234 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1235           210                      215                      220
1237 aag aaa aat gca cac gca tta cct aaa gtg gaa ttt cat gcg agc ggc      720
1238 Lys Lys Asn Ala His Ala Leu Pro Lys Val Glu Phe His Ala Ser Gly
1239 225           230                      235                      240
1241 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1242 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1243           245                      250                      255

```

1315 &lt;210&gt; SEQ ID NO: 19

1316 &lt;211&gt; LENGTH: 768

1317 &lt;212&gt; TYPE: DNA

1318 &lt;213&gt; ORGANISM: H. pylori

1320 &lt;221&gt; NAME/KEY: CDS

1321 &lt;222&gt; LOCATION: (1)..(768)

E--&gt; 1323 &lt;400&gt; SEQUENCE: 19

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1324 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1325 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1326 1           5                      10                      15
1328 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1329 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1330           20                      25                      30
1332 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1333 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1334           35                      40                      45
1336 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1337 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
1338           50                      55                      60

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## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

1340 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1341 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1342 65              70              75              80
1344 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1345 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1346              85              90              95
1348 att tta gcg atc aaa caa caa gta aag gat aaa aac gcc ccc att tta      336
1349 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1350              100              105              110
1352 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gct      384
1353 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1354              115              120              125
1356 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt      432
1357 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1358              130              135              140
1360 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa      480
1361 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
1362 145              150              155              160
1364 act tgc atg cgt tat tat ttc act ccc tta gag att tta cct gaa gtg      528
1365 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
1366              165              170              175
1368 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag      576
1369 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1370              180              185              190
1372 ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc ata ctc atc      624
1373 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile
1374              195              200              205
1376 cat tct ggc gac gct att gta gaa tat ttg caa caa aaa tac gcc ctt      672
1377 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1378              210              215              220
1380 aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1381 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1382 225              230              235              240
1384 gat atg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1385 Asp Met Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1386              245              250              255

```

1458 &lt;210&gt; SEQ ID NO: 21

1459 &lt;211&gt; LENGTH: 768

1460 &lt;212&gt; TYPE: DNA

1461 &lt;213&gt; ORGANISM: H. pylori

1463 &lt;221&gt; NAME/KEY: CDS

1464 &lt;222&gt; LOCATION: (1)..(768)

E--&gt; 1466 &lt;400&gt; SEQUENCE: 21

```

1467 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1468 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1469 1              5              10              15
1471 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc      96
1472 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1473              20              25              30

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*insert <220>*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

1475 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1476 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1477          35                      40                      45
1479 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
1480 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
1481          50                      55                      60
1483 tta ttg att gta gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
1484 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1485 65                      70                      75                      80
1487 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1488 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1489          85                      90                      95
1491 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
1492 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1493          100                     105                     110
1495 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc      384
1496 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1497          115                     120                     125
1499 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
1500 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
1501          130                     135                     140
1503 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
1504 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1505 145                     150                     155                     160
1507 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg      528
1508 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
1509          165                     170                     175
1511 att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
1512 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1513          180                     185                     190
1515 agc tat ttt atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc      624
1516 Ser Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Leu Leu Ile
1517          195                     200                     205
1519 cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1520 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1521          210                     215                     220
1523 aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1524 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1525 225                     230                     235                     240
1527 gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa      768
1528 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1529          245                     250                     255

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1601 &lt;210&gt; SEQ ID NO: 23

1602 &lt;211&gt; LENGTH: 768

1603 &lt;212&gt; TYPE: DNA

1604 &lt;213&gt; ORGANISM: H. pylori

1607 &lt;221&gt; NAME/KEY: CDS

1608 &lt;222&gt; LOCATION: (1)..(768)

E--&gt; 1610 &lt;400&gt; SEQUENCE: 23

*insert (2207)*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1611 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
1612 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1613 1          5          10          15
1615 aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc      96
1616 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
1617          20          25          30
1619 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
1620 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
1621          35          40          45
1623 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga      192
1624 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
1625          50          55          60
1627 tta ttg att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag      240
1628 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
1629 65          70          75          80
1631 atg caa aaa tat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
1632 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
1633          85          90          95
1635 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc ccc att tta      336
1636 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
1637          100          105          110
1639 gtg cta ggg aca aaa gcg acg atc caa tct aac gct tat gat aac gcc      384
1640 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
1641          115          120          125
1643 ctg aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt      432
1644 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
1645          130          135          140
1647 ttt gtg ccc ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa      480
1648 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
1649 145          150          155          160
1651 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528
1652 Thr Cys Met Arg Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
1653          165          170          175
1655 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
1656 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
1657          180          185          190
1659 agc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc      624
1660 Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
1661          195          200          205
1663 cat tct ggc gat gct att gtg gaa tac ttg caa caa aaa tac gcc ctt      672
1664 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1665          210          215          220
1667 aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
1668 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1669 225          230          235          240
1671 gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1672 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1673          245          250          255
1745 <210> SEQ ID NO: 25

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## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

1746 <211> LENGTH: 768  
 1747 <212> TYPE: DNA  
 1748 <213> ORGANISM: H. pylori  
 1750 <221> NAME/KEY: CDS  
 1751 <222> LOCATION: (1)..(768)

*insert <2207*

E--> 1753 <400> SEQUENCE: 25

1754	atg	aaa	ata	ggc	ggt	ttt	gat	agc	ggt	gtg	gga	ggg	ttt	agc	ggt	tta	48
1755	Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1756	1			5						10				15			
1758	aaa	agc	ctt	tta	aaa	gcg	caa	tta	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
1759	Lys	Ser	Leu	Leu	Lys	Ala	Gln	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
1760				20					25					30			
1762	gat	agc	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
1763	Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
1764			35				40				45						
1766	caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	aaa	att	gaa	192
1767	Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu	
1768		50				55				60							
1770	tta	tta	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	ctg	gct	tta	gaa	gag	240
1771	Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
1772	65				70				75					80			
1774	atg	caa	aag	cat	tcc	aaa	atc	ccc	att	gtg	ggc	gtg	att	gag	cca	agc	288
1775	Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
1776				85					90					95			
1778	att	tta	gcg	atc	aaa	caa	caa	gtg	aaa	gat	aaa	aac	acc	cct	att	tta	336
1779	Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Thr	Pro	Ile	Leu	
1780				100					105					110			
1782	gtg	cta	ggg	aca	aaa	gcg	acg	atc	caa	tct	aac	gct	tac	gat	aac	gcc	384
1783	Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
1784			115					120					125				
1786	ctg	aaa	caa	caa	ggc	tat	ttg	aag	gtt	tcg	cat	ttg	gcc	act	tct	ctt	432
1787	Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Lys	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
1788		130				135					140						
1790	ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	tta	gaa	480
1791	Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
1792	145				150				155					160			
1794	act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gaa	atc	tta	cct	gaa	gtg	528
1795	Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
1796				165					170					175			
1798	ggt	att	tta	ggc	tgc	acg	cat	ttt	ccc	ttg	atc	gct	caa	aaa	att	gag	576
1799	Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
1800				180					185					190			
1802	ggc	tat	ttt	atg	gaa	cat	ttt	gcc	ctt	cca	acg	ccc	ccc	cta	ctc	atc	624
1803	Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile	
1804			195					200					205				
1806	cat	tct	ggc	gac	gct	att	gtg	gga	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672
1807	His	Ser	Gly	Asp	Ala	Ile	Val	Gly	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
1808		210					215					220					
1810	aag	aaa	aac	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

1811 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 1812 225 230 235 240  
 1814 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768  
 1815 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 1816 245 250 255  
 1888 <210> SEQ ID NO: 27  
 1889 <211> LENGTH: 768  
 1890 <212> TYPE: DNA  
 1891 <213> ORGANISM: H. pylori  
 1893 <221> NAME/KEY: CDS  
 1894 <222> LOCATION: (1)..(768)  
*insert <2207*

E--> 1896 <400> SEQUENCE: 27  
 1897 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta 48  
 1898 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 1899 1 5 10 15  
 1901 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc 96  
 1902 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly  
 1903 20 25 30  
 1905 gat agc gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 1906 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 1907 35 40 45  
 1909 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa 192  
 1910 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu  
 1911 50 55 60  
 1913 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gaa 240  
 1914 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 1915 65 70 75 80  
 1917 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc 288  
 1918 Met. Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 1919 85 90 95  
 1921 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta 336  
 1922 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 1923 100 105 110  
 1925 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc 384  
 1926 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 1927 115 120 125  
 1929 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432  
 1930 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 1931 130 135 140  
 1933 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa 480  
 1934 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 1935 145 150 155 160  
 1937 act tgc atg cgt tat tat ttc act cca tta gag atc ttg cct gaa gtg 528  
 1938 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 1939 165 170 175  
 1941 gtt att tta ggc tgc acg cat ttt ccc ttg atc gct cac caa att gag 576  
 1942 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu  
 1943 180 185 190  
 1945 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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1946 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
1947          195                200                205
1949 cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt      672
1950 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
1951      210                215                220
1953 aag aaa aac gca tgt gca ttc cct aaa gta gaa ttt cat gcg agc ggc      720
1954 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
1955 225                230                235                240
1957 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
1958 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
1959          245                250                255
2031 <210> SEQ ID NO: 29
2032 <211> LENGTH: 768
2033 <212> TYPE: DNA
2034 <213> ORGANISM: H. pylori
2036 <221> NAME/KEY: CDS
2037 <222> LOCATION: (1)..(768)
E--> 2039 <400> SEQUENCE: 29
2040 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
2041 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
2042 1          5          10          15
2044 aaa agc ctt tta aaa gtg caa tta ttt gat gaa atc atc tat tat ggc      96
2045 Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
2046      20          25          30
2048 gat agt gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
2049 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
2050      35          40          45
2052 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa      192
2053 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
2054      50          55          60
2056 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gga gag      240
2057 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Gly Glu
2058 65          70          75          80
2060 atg caa aag tat tcc aaa atc cct att gtg ggc gtg att gag cca agc      288
2061 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
2062      85          90          95
2064 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
2065 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2066      100         105         110
2068 gta cta ggg aca aaa gcg acg att cga tcc aac gct tat gac aac gcc      384
2069 Val Leu Gly Thr Lys Ala Thr Ile Arg Ser Asn Ala Tyr Asp Asn Ala
2070      115         120         125
2072 ctg aaa caa caa ggc tat ttg aat att tcg cat tta gcc act tct ctt      432
2073 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
2074      130         135         140
2076 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa      480
2077 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
2078 145         150         155         160
2080 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528

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## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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2081 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
2082                165                170                175
2084 gtt att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att gag      576
2085 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
2086                180                185                190
2088 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
2089 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
2090                195                200                205
2092 cat tct ggc gat gct att gtg gaa tat ttg caa caa aaa tac gcc ctt      672
2093 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
2094                210                215                220
2096 aag aaa aac gca tgc gca ttc cct aaa gta gaa ttc cat gcg agc ggc      720
2097 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
2098 225                230                235                240
2100 gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
2101 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
2102                245                250                255
2174 <210> SEQ ID NO: 31
2175 <211> LENGTH: 768
2176 <212> TYPE: DNA
2177 <213> ORGANISM: H. pylori
2179 <221> NAME/KEY: CDS
2180 <222> LOCATION: (1)..(768)
E--> 2182 <400> SEQUENCE: 31
2183 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
2184 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
2185 1                5                10                15
2187 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc      96
2188 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
2189                20                25                30
2191 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
2192 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
2193                35                40                45
2195 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga      192
2196 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
2197                50                55                60
2199 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag      240
2200 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
2201 65                70                75                80
2203 atg caa aag cat tcc aaa atc cct att gtg ggt gtg att gag cca agc      288
2204 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
2205                85                90                95
2207 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta      336
2208 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2209                100               105               110
2211 gtg tta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc      384
2212 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
2213                115               120               125
2215 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt      432

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*insert 2207*

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

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2216 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
2217      130                      135                      140
2219 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa      480
2220 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
2221 145                      150                      155                      160
2223 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528
2224 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
2225                      165                      170                      175
2227 gtt att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att gag      576
2228 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
2229                      180                      185                      190
2231 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc      624
2232 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
2233 195                      200                      205
2235 cat tct ggc gat gct att gtg gaa tat ttg caa caa aaa tac acc ctt      672
2236 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
2237 210                      215                      220
2239 aag aaa aat gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
2240 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
2241 225                      230                      235                      240
2243 gat gtg gtt tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa      768
2244 Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
2245                      245                      250                      255

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2317 &lt;210&gt; SEQ ID NO: 33

2318 &lt;211&gt; LENGTH: 765

2319 &lt;212&gt; TYPE: DNA

2320 &lt;213&gt; ORGANISM: H. pylori

2322 &lt;221&gt; NAME/KEY: CDS

2323 &lt;222&gt; LOCATION: (1)..(765)

E--&gt; 2325 &lt;400&gt; SEQUENCE: 33

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2326 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta      48
2327 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
2328 1      5      10      15
2330 aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc      96
2331 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
2332      20      25      30
2334 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag      144
2335 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
2336      35      40      45
2338 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa      192
2339 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
2340      50      55      60
2342 tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag      240
2343 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
2344 65      70      75      80
2346 atg caa aag cat tcc aaa atc cct gtt gtg ggc gtg att gag cca agc      288
2347 Met Gln Lys His Ser Lys Ile Pro Val Val Gly Val Ile Glu Pro Ser
2348      85      90      95
2350 att tta gcg atc aaa cgg caa gtg aaa gat aaa aac gcc cct att ttg      336

```

## RAW SEQUENCE LISTING

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:57

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

```

2351 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
2352           100                      105                      110
2354 gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gat aac gcc      384
2355 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
2356           115                      120                      125
2358 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt      432
2359 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
2360           130                      135                      140
2362 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa      480
2363 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
2364 145                      150                      155                      160
2366 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg      528
2367 Thr Cys Met Arg Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
2368           165                      170                      175
2370 gtt att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag      576
2371 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
2372           180                      185                      190
2374 ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc      624
2375 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
2376           195                      200                      205
2378 cat tct ggc gat gct att gtg gaa tat ttg caa caa aat tac gcc ctt      672
2379 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu
2380           210                      215                      220
2382 aag aaa aac gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc      720
2383 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
2384 225                      230                      235                      240
2386 gat gtg gtt tgg cta gaa aaa caa gct aaa gaa tgg ctt aaa ttg      765
2387 Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
2388           245                      250                      255
3614 <210> SEQ ID NO: 75
3615 <211> LENGTH: 19
3616 <212> TYPE: DNA
3617 <213> ORGANISM: primer
3619 <400> SEQUENCE: 75
E--> 3620 tfatgcaaca aatggacga

```

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*invalid response - see item 10 on Error Summary Sheet*

*invalid nucleotide designator*

*same error in sequence 76*

## VERIFICATION SUMMARY

DATE: 10/20/2006

PATENT APPLICATION: US/10/729,571C

TIME: 09:16:58

Input Set : A:\100966-2P US Sequence Listing.txt

Output Set: N:\CRF4\10202006\J729571C.raw

L:36 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1  
L:179 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3  
L:322 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5  
L:465 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7  
L:608 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9  
L:751 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11  
L:894 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13  
L:1037 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15  
L:1180 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17  
L:1323 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:19  
L:1466 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:21  
L:1610 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:23  
L:1753 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:25  
L:1896 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:27  
L:2039 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:29  
L:2182 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:31  
L:2325 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:33  
L:3620 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:24 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (76) Counted (97)

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<210> 97 last sequence in submitted file  
<211> 32  
<212> PRT  
<213> Enterococcus faecium

<400> 97

Lys Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu  
1 5 10 15

Arg Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu Ile Asp  
20 25 30